

Query= SEQ ID NO:6
 (1110 letters)

Sequences producing significant alignments:	Score (bits)	E Value
---	-----------------	------------

AC113382.2.1.166870	<u>1084</u>	0.0
---------------------	-------------	-----

>AC113382.2.1.166870
 Length = 166870

Score = 1084 bits (547), Expect = 0.0
 Identities = 547/547 (100%)
 Strand = Plus / Minus

Query: 564	ggcagtgagagccaccatgaaaaggacatgcaaattgcatggcatctctgggagctgcag	623
Sbjct: 80777	ggcagtgagagccaccatgaaaaggacatgcaaattgcatggcatctctgggagctgcag	80718

Query: 624	catacagacatgctggctgcagctggctgaattccgggagatgggagactacctaaaggc	683
Sbjct: 80717	catacagacatgctggctgcagctggctgaattccgggagatgggagactacctaaaggc	80658

Query: 684	caagtatgaccaggcgctgaaaattgaaatggataagcggcagctgagagctgggaacag	743
Sbjct: 80657	caagtatgaccaggcgctgaaaattgaaatggataagcggcagctgagagctgggaacag	80598

Query: 744	cgccgagggccactgggtgcccgcctgaggccttccttcctagcgcagaggcggaactgat	803
Sbjct: 80597	cgccgagggccactgggtgcccgcctgaggccttccttcctagcgcagaggcggaactgat	80538

Query: 804	cttttttagaggaatcaccagattactgtacctgcaattccagcctgggcatctatggcac	863
Sbjct: 80537	cttttttagaggaatcaccagattactgtacctgcaattccagcctgggcatctatggcac	80478

Query: 864	agagggctcgtgagtgacctacagaacagccacaacacatccaggtgggagcgacgtagctg	923
Sbjct: 80477	agagggctcgtgagtgacctacagaacagccacaacacatccaggtgggagcgacgtagctg	80418

Query: 924	tgggcgcctgtgcactgagtggtggctgcaggtggaagagaggaaaactgaggtcataag	983
Sbjct: 80417	tgggcgcctgtgcactgagtggtggctgcaggtggaagagaggaaaactgaggtcataag	80358

Query: 984	cagctgtaactgcaaattccagtggtgctgtacgggtcaagtgtgaccagtgtaggcatgt	1043
Sbjct: 80357	cagctgtaactgcaaattccagtggtgctgtacgggtcaagtgtgaccagtgtaggcatgt	80298

Query: 1044 ggtgagcaagtattactgcgacgctccccaggcagtgcccagtcctgggtaagggcag 1103
|||||
Sbjct: 80297 ggtgagcaagtattactgcgacgctccccaggcagtgcccagtcctgggtaagggcag 80238

Query: 1104 tgcctga 1110
|||||
Sbjct: 80237 tgcctga 80231

Score = 311 bits (157), Expect = 5e-82
Identities = 157/157 (100%)
Strand = Plus / Minus

Query: 1 atgctgtgctgcattcagtgccctctgacctggaagtcctttcccaaccctcactccttgc 60
|||||
Sbjct: 87176 atgctgtgctgcattcagtgccctctgacctggaagtcctttcccaaccctcactccttgc 87117

Query: 61 caaggaggccccattgtctcatccccattcacctctgacctactttttctctttttggt 120
|||||
Sbjct: 87116 caaggaggccccattgtctcatccccattcacctctgacctactttttctctttttggt 87057

Query: 121 aggtcagtgaacaatttcctgataacaggtcccaagg 157
|||||
Sbjct: 87056 aggtcagtgaacaatttcctgataacaggtcccaagg 87020

Score = 289 bits (146), Expect = 2e-75
Identities = 146/146 (100%)
Strand = Plus / Minus

Query: 420 aggaggccatggctggatctggggaggctgcagcgacaatgtggaatttggggaaaggat 479
|||||
Sbjct: 82379 aggaggccatggctggatctggggaggctgcagcgacaatgtggaatttggggaaaggat 82320

Query: 480 ctccaaactctttgtggacagtttgaggagaaggggaaggatgccagagccctgatgaatct 539
|||||
Sbjct: 82319 ctccaaactctttgtggacagtttgaggagaaggggaaggatgccagagccctgatgaatct 82260

Query: 540 tcacaacaacagggccggcagactgg 565
|||||
Sbjct: 82259 tcacaacaacagggccggcagactgg 82234

Score = 280 bits (141), Expect = 2e-72
Identities = 141/141 (100%)
Strand = Plus / Minus

Query: 155 aggcctatctgacctacacgactagtgtggccttgggtgcccagagtggcatcgaggagt 214
|||||
Sbjct: 86808 aggcctatctgacctacacgactagtgtggccttgggtgcccagagtggcatcgaggagt 86749

Query: 215 gcaagttccagtttgcttgggaacgctggaactgccctgaaaatgctcttcagctctcca 274
|||||
Sbjct: 86748 gcaagttccagtttgcttgggaacgctggaactgccctgaaaatgctcttcagctctcca 86689

Query: 275 cccacaacaggctgagaagtg 295
|||||
Sbjct: 86688 cccacaacaggctgagaagtg 86668

Score = 254 bits (128), Expect = 1e-64
Identities = 128/128 (100%)
Strand = Plus / Minus

Query: 295 gctaccagagagacttccttcatacatgctatcagctctgctggagtcatgtacatcatc 354
|||||
Sbjct: 83499 gctaccagagagacttccttcatacatgctatcagctctgctggagtcatgtacatcatc 83440

Query: 355 accaagaactgtagcatgggtgacttcgaaaactgtggctgtgatgggtcaaacaatgga 414
|||||
Sbjct: 83439 accaagaactgtagcatgggtgacttcgaaaactgtggctgtgatgggtcaaacaatgga 83380

Query: 415 aaaacagg 422
|||||
Sbjct: 83379 aaaacagg 83372



Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

Search for

Limits

Preview/Index

History

Clipboard

Details

Show:

☐ 1: [AC113382](#). Homo sapiens chro...[gi:27923635][Links](#)

LOCUS AC113382 166870 bp DNA linear PRI 28-JAN-2003

DEFINITION Homo sapiens chromosome 5 clone RP11-325L7, complete sequence.

ACCESSION AC113382

VERSION AC113382.2 GI:27923635

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 166870)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 166870)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 166870)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USACOMMENT On Jan 28, 2003 this sequence version replaced [gi:19033496](#).

Draft Sequence Produced by DOE Joint Genome Institute

[www.jgi.doe.gov](#)

Finishing Completed at Stanford Human Genome Center

[www-shgc.stanford.edu](#)

Quality: Phrap Quality >=40 99.8% of Sequence;

Estimated Total Number of Errors is 0.2.

FEATURES Location/Qualifiers

source

1..166870

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="RP11-325L7"

ORIGIN

```
1 gaattctggt ttatacttag ttatgatact ggatgattaa aaaatagcag aagttatcta
61 tgattaagtg gtaaaagcaa gtaggagagg ggataaatgt tatgttattt gaatatgaat
121 tttttttttt caattttcca cagacggaaa cgaggtgaaa agggagaagt ggtggaaact
181 gttgaagatg ttattgttcg gaaattgact gctgagcgag ttgaagaact aaagaaagtg
241 ataaaggaaa cccaggagag ataataggtac ttatcagaga gaatgcaaaa aaattgagaa
301 agacataagg gactgtcttc tggtagctgg cagaactttt aaaatagcag attaaaaaac
361 ccagtctacc tacctctctt tcttcctata gacggctaaa gagagatgca gaactaatc
421 aagctggaca catggacagc agactggatg agctttgcaa tgacattgca acgtgggtta
481 tattatattg ttcttctgtg cttctttctt tttaccctct tttccctca agtaatctgg
541 cttatttcct ccaattgccg tccctttaga cttgagacag attctggaag gggaaagctg
601 caaagtgggt tggtagctgg gaggggggag tgagtcttag aaggtaatat aatgggacat
```